

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

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(ii) TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
Uses Therefor

(iii) NUMBER OF SEQUENCES: 31

15

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/280,757; 08/101,624; 08/109,393;
08/147,773
(B) FILING DATE: 26-JUL-1994; 26-JUL-1993; 19-AUG-1993; 03-NOV-
1993

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.
(B) REGISTRATION NUMBER: 36,207
(C) REFERENCE/DOCKET NUMBER: RPI-004CP3

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 107..1093

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | |
|----|---|-----|
| | CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT | 60 |
| 20 | GAGTGGGGTC ATTTCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC | 115 |
| | Met Asp Pro | |
| | 1 | |
| 25 | CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG | 163 |
| | Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu | |
| | 5 10 15 | |
| 30 | CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT | 211 |
| | Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr | |
| | 20 25 30 35 | |
| 35 | GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT | 259 |
| | Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser | |
| | 40 45 50 | |
| 40 | GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG | 307 |
| | Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu | |
| | 55 60 65 | |
| 45 | GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG | 355 |
| | Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met | |
| | 70 75 80 | |
| 50 | GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT | 403 |
| | Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn | |
| | 85 90 95 | |
| 55 | CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA | 451 |
| | Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys | |
| | 100 105 110 115 | |
| | AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA | 499 |
| | Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser | |
| | 120 125 130 | |

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| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|------------|------------|---------|-----|-----|-----|-----|-----|-----|-----|------|
| | GTG | CTT | GCT | AAC | TTC | AGT | CAA | CCT | GAA | ATA | GTA | CCA | ATT | TCT | AAT | ATA | 547 |
| | Val | Leu | Ala | Asn | Phe | Ser | Gln | Pro | Glu | Ile | Val | Pro | Ile | Ser | Asn | Ile | |
| | | | | 135 | | | | | 140 | | | | | 145 | | | |
| 5 | ACA | GAA | AAT | GTG | TAC | ATA | AAT | TTG | ACC | TGC | TCA | TCT | ATA | CAC | GGT | TAC | 595 |
| | Thr | Glu | Asn | Val | Tyr | Ile | Asn | Leu | Thr | Cys | Ser | Ser | Ile | His | Gly | Tyr | |
| | | | 150 | | | | | 155 | | | | | 160 | | | | |
| 10 | CCA | GAA | CCT | AAG | AAG | ATG | AGT | GTT | TTG | CTA | AGA | ACC | AAG | AAT | TCA | ACT | 643 |
| | Pro | Glu | Pro | Lys | Lys | Met | Ser | Val | Leu | Leu | Arg | Thr | Lys | Asn | Ser | Thr | |
| | | 165 | | | | | 170 | | | | | 175 | | | | | |
| 15 | ATC | GAG | TAT | GAT | GGT | ATT | ATG | CAG | AAA | TCT | CAA | GAT | AAT | GTC | ACA | GAA | 691 |
| | Ile | Glu | Tyr | Asp | Gly | Ile | Met | Gln | Lys | Ser | Gln | Asp | Asn | Val | Thr | Glu | |
| | 180 | | | | | 185 | | | | | 190 | | | | | 195 | |
| 20 | CTG | TAC | GAC | GTT | TCC | ATC | AGC | TTG | TCT | GTT | TCA | TTC | CCT | GAT | GTT | ACG | 739 |
| | Leu | Tyr | Asp | Val | Ser | Ile | Ser | Leu | Ser | Val | Ser | Phe | Pro | Asp | Val | Thr | |
| | | | | | 200 | | | | | 205 | | | | | 210 | | |
| 25 | AGC | AAT | ATG | ACC | ATC | TTC | TGT | ATT | CTG | GAA | ACT | GAC | AAG | ACG | CGG | CTT | 787 |
| | Ser | Asn | Met | Thr | Ile | Phe | Cys | Ile | Leu | Glu | Thr | Asp | Lys | Thr | Arg | Leu | |
| | | | | 215 | | | | | 220 | | | | | 225 | | | |
| 30 | TTA | TCT | TCA | CCT | TTC | TCT | ATA | GAG | CTT | GAG | GAC | CCT | CAG | CCT | CCC | CCA | 835 |
| | Leu | Ser | Ser | Pro | Phe | Ser | Ile | Glu | Leu | Glu | Asp | Pro | Gln | Pro | Pro | Pro | |
| | | | 230 | | | | | 235 | | | | | 240 | | | | |
| 35 | GAC | CAC | ATT | CCT | TGG | ATT | ACA | GCT | GTA | CTT | CCA | ACA | GTT | ATT | ATA | TGT | 883 |
| | Asp | His | Ile | Pro | Trp | Ile | Thr | Ala | Val | Leu | Pro | Thr | Val | Ile | Ile | Cys | |
| | | 245 | | | | | 250 | | | | | 255 | | | | | |
| 40 | GTG | ATG | GTT | TTC | TGT | CTA | ATT | CTA | TGG | AAA | TGG | AAG | AAG | AAG | AAG | CGG | 931 |
| | Val | Met | Val | Phe | Cys | Leu | Ile | Leu | Trp | Lys | Trp | Lys | Lys | Lys | Lys | Arg | |
| | 260 | | | | | 265 | | | | | 270 | | | | | 275 | |
| 45 | CCT | CGC | AAC | TCT | TAT | AAA | TGT | GGA | ACC | AAC | ACA | ATG | GAG | AGG | GAA | GAG | 979 |
| | Pro | Arg | Asn | Ser | Tyr | Lys | Cys | Gly | Thr | Asn | Thr | Met | Glu | Arg | Glu | Glu | |
| | | | | | 280 | | | | | 285 | | | | | 290 | | |
| 50 | AGT | GAA | CAG | ACC | AAG | AAA | AGA | GAA | AAA | ATC | CAT | ATA | CCT | GAA | AGA | TCT | 1027 |
| | Ser | Glu | Gln | Thr | Lys | Lys | Arg | Glu | Lys | Ile | His | Ile | Pro | Glu | Arg | Ser | |
| | | | | 295 | | | | 300 | | | | | | 305 | | | |
| 45 | GAT | GAA | GCC | CAG | CGT | GTT | TTT | AAA | AGT | TCG | AAG | ACA | TCT | TCA | TGC | GAC | 1075 |
| | Asp | Glu | Ala | Gln | Arg | Val | Phe | Lys | Ser | Ser | Lys | Thr | Ser | Ser | Cys | Asp | |
| | | | 310 | | | | | 315 | | | | | 320 | | | | |
| 50 | AAA | AGT | GAT | ACA | TGT | TTT | TAATTAAAGA | GTAAAGCCCA | AAAAAAA | | | | | | | | 1120 |
| | Lys | Ser | Asp | Thr | Cys | Phe | | | | | | | | | | | |
| | | | | 325 | | | | | | | | | | | | | |

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Gln | Cys | Thr | Met | Gly | Leu | Ser | Asn | Ile | Leu | Phe | Val | Met | 1 | 5 | 10 | 15 |
| Ala | Phe | Leu | Leu | Ser | Gly | Ala | Ala | Pro | Leu | Lys | Ile | Gln | Ala | Tyr | Phe | 20 | 25 | 30 | |
| Asn | Glu | Thr | Ala | Asp | Leu | Pro | Cys | Gln | Phe | Ala | Asn | Ser | Gln | Asn | Gln | 35 | 40 | 45 | |
| Ser | Leu | Ser | Glu | Leu | Val | Val | Phe | Trp | Gln | Asp | Gln | Glu | Asn | Leu | Val | 50 | 55 | 60 | |
| Leu | Asn | Glu | Val | Tyr | Leu | Gly | Lys | Glu | Lys | Phe | Asp | Ser | Val | His | Ser | 65 | 70 | 75 | 80 |
| Lys | Tyr | Met | Gly | Arg | Thr | Ser | Phe | Asp | Ser | Asp | Ser | Trp | Thr | Leu | Arg | 85 | 90 | 95 | |
| Leu | His | Asn | Leu | Gln | Ile | Lys | Asp | Lys | Gly | Leu | Tyr | Gln | Cys | Ile | Ile | 100 | 105 | 110 | |
| His | His | Lys | Lys | Pro | Thr | Gly | Met | Ile | Arg | Ile | His | Gln | Met | Asn | Ser | 115 | 120 | 125 | |
| Glu | Leu | Ser | Val | Leu | Ala | Asn | Phe | Ser | Gln | Pro | Glu | Ile | Val | Pro | Ile | 130 | 135 | 140 | |
| Ser | Asn | Ile | Thr | Glu | Asn | Val | Tyr | Ile | Asn | Leu | Thr | Cys | Ser | Ser | Ile | 145 | 150 | 155 | 160 |
| His | Gly | Tyr | Pro | Glu | Pro | Lys | Lys | Met | Ser | Val | Leu | Leu | Arg | Thr | Lys | 165 | 170 | 175 | |
| Asn | Ser | Thr | Ile | Glu | Tyr | Asp | Gly | Ile | Met | Gln | Lys | Ser | Gln | Asp | Asn | 180 | 185 | 190 | |
| Val | Thr | Glu | Leu | Tyr | Asp | Val | Ser | Ile | Ser | Leu | Ser | Val | Ser | Phe | Pro | 195 | 200 | 205 | |
| Asp | Val | Thr | Ser | Asn | Met | Thr | Ile | Phe | Cys | Ile | Leu | Glu | Thr | Asp | Lys | 210 | 215 | 220 | |
| Thr | Arg | Leu | Leu | Ser | Ser | Pro | Phe | Ser | Ile | Glu | Leu | Glu | Asp | Pro | Gln | 225 | 230 | 235 | 240 |

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Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
 245 250 255

5 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
 260 265 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
 275 280 285

10 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
 290 295 300

15 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
 305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
 325

20 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAATACGACT CACTATAGGG

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAAGGTTCCCT TCACAAAG

18

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: oligonucleotide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTGGTAGGT ATGGAAGATC C

21

(2) INFORMATION FOR SEQ ID NO:6:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: oligonucleotide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCGAATCA TTCCTGTGGG C

21

(2) INFORMATION FOR SEQ ID NO:7:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGCCCACA GGAATGATTC G

21

45 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCTCAAAAC CAAAGCCTGA G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTAGGTCACA GCAGAAGCAG C

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTGGAAACT GACAAGACGC G

21

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCAGGCTTT GGTTTTGAGA G

21

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662201"9T52460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTCTCTTC CCTCTCCATT G 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACAAGCTGA TGGAAACGTC G 21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAATGGAGAG GGAAGAGAGT G 21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

66220T"9T52460

(ii) MOLECULE TYPE: oligonucleotide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTTAGAGCA CA

12

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCTAAAG

8

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

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(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Met Gly Arg Thr Ser Phe Asp

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 111..1040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | |
|----|---|---------|
| 20 | CCCACGCGTC CGGGAGCAAG CAGACGCGTA AGAGTGGCTC CTGTAGGCAG CACGGACTTG | 60 |
| | AACAACCAGA CTCCTGTAGA CGTGTTCAG AACTTACGGA AGCACCCACG ATG GAC | 116 |
| | | Met Asp |
| | | 1 |
| 25 | CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG | 164 |
| | Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu | |
| | 5 10 15 | |
| 30 | CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG | 212 |
| | Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly | |
| | 20 25 30 | |
| 35 | ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG | 260 |
| | Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu | |
| | 35 40 45 50 | |
| 40 | AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC | 308 |
| | Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr | |
| | 55 60 65 | |
| | GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC | 356 |
| | Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr | |
| | 70 75 80 | |
| 45 | CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC | 404 |
| | Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His | |
| | 85 90 95 | |
| 50 | AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA | 452 |
| | Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys | |
| | 100 105 110 | |
| 55 | AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG | 500 |
| | Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu | |
| | 115 120 125 130 | |

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| | | |
|----|---|------|
| | TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT | 548 |
| | Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn | |
| | 135 140 145 | |
| 5 | GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT | 596 |
| | Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly | |
| | 150 155 160 | |
| 10 | CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT | 644 |
| | His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn | |
| | 165 170 175 | |
| 15 | GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG | 692 |
| | Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu | |
| | 180 185 190 | |
| 20 | TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG | 740 |
| | Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp | |
| | 195 200 205 210 | |
| 25 | CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC | 788 |
| | His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser | |
| | 215 220 225 | |
| 30 | TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT | 836 |
| | Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr | |
| | 230 235 240 | |
| 35 | TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG | 884 |
| | Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met | |
| | 245 250 255 | |
| 40 | CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC | 932 |
| | Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro | |
| | 260 265 270 | |
| 45 | AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG | 980 |
| | Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu | |
| | 275 280 285 290 | |
| 50 | ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA | 1028 |
| | Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro | |
| | 295 300 305 | |
| 55 | AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT | 1077 |
| | Asn Ala Glu | |
| 60 | TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA | 1137 |
| | ATTCTACAGT TGAATAATTA AAGAAC | 1163 |

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr
1 5 10 15
Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe
20 25 30
Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
35 40 45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
50 55 60
Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
25 65 70 75 80
Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
85 90 95
Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
30 100 105 110
Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
115 120 125
Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
35 130 135 140
Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
40 145 150 155 160
Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175
Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
45 180 185 190
Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
195 200 205
Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
50 210 215 220
Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
55 225 230 235 240

0045516.10369

Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
245 250 255

5 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
275 280 285

10 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
290 295 300

Lys Pro Asn Ala Glu
15 305

(2) INFORMATION FOR SEQ ID NO:24:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: oligonucleotide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACATAAGCCT GAGTGAGCTG G

21

35 (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGATGAGCA GCATCACAAG G

50

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 TGGTCGAGTG AGTCCGAATA C

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

30 GACGAGTAGT AACATACAGT G

21

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

094541029
6622019T52460

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: Homo sapien
(F) TISSUE TYPE: lymphoid
(G) CELL TYPE: B cell
(H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

- 10 (A) LIBRARY: cDNA in pCDM8 vector
(B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

- 15 (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

- 20 (A) NAME/KEY: Open reading frame (translated region)
(B) LOCATION: 318 to 1181 bp
(C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

- 25 (A) NAME/KEY: Alternate polyadenylation signal
(B) LOCATION: 1474 to 1479 bp
(C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

- 30 (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
35 WHITMAN, JAMES F.
NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
40
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
45 (G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES In SEQ ID NO:28: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAAGCAAGCT 120
55 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180

GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240

TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGGCTTT CACTTTTGAC 300

5 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
-30 -25

10 AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
-20 -15 -10

15 TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
-5 1 5 10

20 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
15 20 25

25 CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
30 35 40

30 ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
45 50 55

35 TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
60 65 70

40 TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
75 80 85 90

45 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
95 100 105

50 GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT 785
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
110 115 120

55

55220T" 9T55220T

| | | | | | | | | | | | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | ATT | AGA | AGG | ATA | ATT | TGC | TCA | ACC | TCT | GGA | GGT | TTT | CCA | GAG | CCT | CAC | 833 |
| | Ile | Arg | Arg | Ile | Ile | Cys | Ser | Thr | Ser | Gly | Gly | Phe | Pro | Glu | Pro | His | |
| | | | 125 | | | | | 130 | | | | | 135 | | | | |
| 5 | CTC | TCC | TGG | TTG | GAA | AAT | GGA | GAA | GAA | TTA | AAT | GCC | ATC | AAC | ACA | ACA | 881 |
| | Leu | Ser | Trp | Leu | Glu | Asn | Gly | Glu | Glu | Leu | Asn | Ala | Ile | Asn | Thr | Thr | |
| | | | 140 | | | | 145 | | | | | 150 | | | | | |
| 10 | GTT | TCC | CAA | GAT | CCT | GAA | ACT | GAG | CTC | TAT | GCT | GTT | AGC | AGC | AAA | CTG | 929 |
| | Val | Ser | Gln | Asp | Pro | Glu | Thr | Glu | Leu | Tyr | Ala | Val | Ser | Ser | Lys | Leu | |
| | 155 | | | | | 160 | | | | | 165 | | | | | 170 | |
| 15 | GAT | TTC | AAT | ATG | ACA | ACC | AAC | CAC | AGC | TTC | ATG | TGT | CTC | ATC | AAG | TAT | 977 |
| | Asp | Phe | Asn | Met | Thr | Thr | Asn | His | Ser | Phe | Met | Cys | Leu | Ile | Lys | Tyr | |
| | | | | | 175 | | | | | 180 | | | | | 185 | | |
| 20 | GGA | CAT | TTA | AGA | GTG | AAT | CAG | ACC | TTC | AAC | TGG | AAT | ACA | ACC | AAG | CAA | 1025 |
| | Gly | His | Leu | Arg | Val | Asn | Gln | Thr | Phe | Asn | Trp | Asn | Thr | Thr | Lys | Gln | |
| | | | | 190 | | | | | 195 | | | | | 200 | | | |
| 25 | GAG | CAT | TTT | CCT | GAT | AAC | CTG | CTC | CCA | TCC | TGG | GCC | ATT | ACC | TTA | ATC | 1073 |
| | Glu | His | Phe | Pro | Asp | Asn | Leu | Leu | Pro | Ser | Trp | Ala | Ile | Thr | Leu | Ile | |
| | | | 205 | | | | 210 | | | | | 215 | | | | | |
| 30 | TCA | GTA | AAT | GGA | ATT | TTT | GTG | ATA | TGC | TGC | CTG | ACC | TAC | TGC | TTT | GCC | 1121 |
| | Ser | Val | Asn | Gly | Ile | Phe | Val | Ile | Cys | Cys | Leu | Thr | Tyr | Cys | Phe | Ala | |
| | | 220 | | | | | 225 | | | | | 230 | | | | | |
| 35 | CCA | AGA | TGC | AGA | GAG | AGA | AGG | AGG | AAT | GAG | AGA | TTG | AGA | AGG | GAA | AGT | 1169 |
| | Pro | Arg | Cys | Arg | Glu | Arg | Arg | Arg | Asn | Glu | Arg | Leu | Arg | Arg | Glu | Ser | |
| | 235 | | | | | 240 | | | | 245 | | | | | 250 | | |
| 40 | GTA | CGC | CCT | GTA | TAACAGTGTG | CGCAGAAGCA | AGGGGCTGAA | AAGATCTGAA | | | | | | | | | 1221 |
| | Val | Arg | Pro | Val | | | | | | | | | | | | | |
| 45 | GGTAGCCTCC | GTCATCTCTT | CTGGGATACA | TGGATCGTGG | GGATCATGAG | GCATTCTTCC | | | | | | | | | | | 1281 |
| | CTTAACAAAT | TTAAGCTGTT | TTACCCACTA | CCTCACCTTC | TTAAAAACCT | CTTTCAGATT | | | | | | | | | | | 1341 |
| 50 | AAGCTGAACA | GTTACAAGAT | GGCTGGCATC | CCTCTCCTTT | CTCCCCATAT | GCAATTTGCT | | | | | | | | | | | 1401 |
| | TAATGTAACC | TCTTCTTTTG | CCATGTTTCC | ATTCTGCCAT | CTTGAATTGT | CTTGTCAGCC | | | | | | | | | | | 1461 |
| 55 | | | | | | | | | | | | | | | | | |

66220T" 9T552466

AATTCATTAT CTATTAAACA CTAATTTGAG
1491

5

(3) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein

20

(ix) FEATURE:

- (A) NAME/KEY: signal sequence
- (B) LOCATION: -34 to -1
- (C) IDENTIFICATION METHOD: amino terminal sequencing of
soluble protein
- (D) OTHER INFORMATION: hydrophobic

25

(ix) FEATURE:

- (A) NAME/KEY: extracellular domain
- (B) LOCATION: 1 to 208
- (C) IDENTIFICATION METHOD: similarity with known
sequence

30

35

(ix) FEATURE:

- (A) NAME/KEY: transmembrane domain
- (B) LOCATION: 209 to 235
- (C) IDENTIFICATION METHOD: similarity with known
sequence

40

(ix) FEATURE:

- (A) NAME/KEY: intracellular domain
- (B) LOCATION: 236 to 254
- (C) IDENTIFICATION METHOD: similarity with known
sequence

45

50

0945516 10629

(ix) FEATURE:

- 5 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 19 to 21
(C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- 10 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 55 to 57
(C) IDENTIFICATION METHOD: similarity with known sequence

15

(ix) FEATURE:

- 20 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 64 to 66
(C) IDENTIFICATION METHOD: similarity with known sequence

25 (ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 152 to 154
(C) IDENTIFICATION METHOD: similarity with known sequence

30

(ix) FEATURE:

- 35 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 173 to 175
(C) IDENTIFICATION METHOD: similarity with known sequence

40

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 177 to 179
(C) IDENTIFICATION METHOD: similarity with known sequence

45

(ix) FEATURE:

- 50 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 192 to 194
(C) IDENTIFICATION METHOD: similarity with known sequence

55

66207 9752460

(ix) FEATURE:

- 5 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 198 to 200
(C) IDENTIFICATION METHOD: similarity with known sequence

10 (ix) FEATURE:

- (A) NAME/KEY: Ig V-set domain
(B) LOCATION: 1 to 104
15 (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- 20 (A) NAME/KEY: Ig C-set domain
(B) LOCATION: 105 to 202
(C) IDENTIFICATION METHOD: similarity with known sequence

25 (x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
30 LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With
35 Unique Expression On Activated And Neoplastic B Cells
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
40 (G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES IN SEQUENCE ID NO:29: From -26 to 262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

45

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Met | Gly | His | Thr | Arg | Arg | Gln | Gly | Thr | Ser | Pro | Ser | Lys | Cys | Pro | Tyr | |
| | | | | | -30 | | | | | -25 | | | | | -20 | | |
| 5 | Leu | Asn | Phe | Phe | Gln | Leu | Leu | Val | Leu | Ala | Gly | Leu | Ser | His | Phe | Cys | |
| | | | | -15 | | | | | -10 | | | | | -5 | | | |
| | Ser | Gly | Val | Ile | His | Val | Thr | Lys | Glu | Val | Lys | Glu | Val | Ala | Thr | Leu | |
| | -1 | | 1 | | | | | 5 | | | | 10 | | | | | |
| 10 | Ser | Cys | Gly | His | Asn | Val | Ser | Val | Glu | Glu | Leu | Ala | Gln | Thr | Arg | Ile | |
| | 15 | | | | | 20 | | | | | 25 | | | | | 30 | |
| | Tyr | Trp | Gln | Lys | Glu | Lys | Lys | Met | Val | Leu | Thr | Met | Met | Ser | Gly | Asp | |
| | | | | | 35 | | | | | 40 | | | | | 45 | | |
| 15 | Met | Asn | Ile | Trp | Pro | Glu | Tyr | Lys | Asn | Arg | Thr | Ile | Phe | Asp | Ile | Thr | |
| | | | | 50 | | | | | 55 | | | | | 60 | | | |
| | Asn | Asn | Leu | Ser | Ile | Val | Ile | Leu | Ala | Leu | Arg | Pro | Ser | Asp | Glu | Gly | |
| 20 | | | 65 | | | | | 70 | | | | | 75 | | | | |
| | Thr | Tyr | Glu | Cys | Val | Val | Leu | Lys | Tyr | Glu | Lys | Asp | Ala | Phe | Lys | Arg | |
| | 80 | | | | | | 85 | | | | | 90 | | | | | |
| 25 | Glu | His | Leu | Ala | Glu | Val | Thr | Leu | Ser | Val | Lys | Ala | Asp | Phe | Pro | Thr | |
| | 95 | | | | | 100 | | | | | 105 | | | | | 110 | |
| | Pro | Ser | Ile | Ser | Asp | Phe | Glu | Ile | Pro | Thr | Ser | Asn | Ile | Arg | Arg | Ile | |
| | | | | | 115 | | | | | 120 | | | | | 125 | | |
| 30 | Ile | Cys | Ser | Thr | Ser | Gly | Gly | Phe | Pro | Glu | Pro | His | Leu | Ser | Trp | Leu | |
| | | | | 130 | | | | | 135 | | | | | 140 | | | |
| | Glu | Asn | Gly | Glu | Glu | Leu | Asn | Ala | Ile | Asn | Thr | Thr | Val | Ser | Gln | Asp | |
| 35 | | | 145 | | | | | 150 | | | | | 155 | | | | |
| | Pro | Glu | Thr | Glu | Leu | Tyr | Ala | Val | Ser | Ser | Lys | Leu | Asp | Phe | Asn | Met | |
| | | 160 | | | | | 165 | | | | | 170 | | | | | |
| 40 | Thr | Thr | Asn | His | Ser | Phe | Met | Cys | Leu | Ile | Lys | Tyr | Gly | His | Leu | Arg | |
| | 175 | | | | | 180 | | | | | 185 | | | | | 190 | |
| | Val | Asn | Gln | Thr | Phe | Asn | Trp | Asn | Thr | Thr | Lys | Gln | Glu | His | Phe | Pro | |
| 45 | | | | | 195 | | | | | 200 | | | | | 205 | | |
| | Asp | Asn | Leu | Leu | Pro | Ser | Trp | Ala | Ile | Thr | Leu | Ile | Ser | Val | Asn | Gly | |
| | | | 210 | | | | | | 215 | | | | | 220 | | | |
| 50 | Ile | Phe | Val | Ile | Cys | Cys | Leu | Thr | Tyr | Cys | Phe | Ala | Pro | Arg | Cys | Arg | |
| | | 225 | | | | | | 230 | | | | | 235 | | | | |
| | Glu | Arg | Arg | Arg | Asn | Glu | Arg | Leu | Arg | Arg | Glu | Ser | Val | Arg | Pro | Val | |
| | 240 | | | | | | 245 | | | | | 250 | | | | | |
| 55 | | | | | | | | | | | | | | | | | |

045546 1033

(4) INFORMATION FOR SEQ ID NO:30:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(ii) MOLECULAR TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus
- (D) DEVELOPMENTAL STAGE: germ line
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B lymphocyte
- (H) CELL LINE: 70Z and A20

20

(vii) IMMEDIATE SOURCE:

25

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7 #'s 1 and 29

(ix) FEATURE:

30

- (A) NAME/KEY: translated region
- (B) LOCATION: 249 to 1166 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

35

- (A) NAME/KEY: Alternate ATG initiation codons
- (B) LOCATION: 225 to 227 and 270 to 272
- (C) IDENTIFICATION METHOD: similarity to other pattern

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

045541039

| | | |
|----|--|-----|
| | GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC | 60 |
| | TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG | 120 |
| 5 | TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA | 180 |
| | GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT | 240 |
| 10 | CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu | 290 |
| | -35 -30 -25 | |
| 15 | AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg | 338 |
| | -20 -15 -10 | |
| 20 | CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val | 386 |
| | -5 -1 1 5 | |
| 25 | AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp | 434 |
| | 10 15 20 25 | |
| 30 | GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu | 482 |
| | 30 35 40 | |
| 35 | TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg | 530 |
| | 45 50 55 | |
| 40 | ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val | 578 |
| | 60 65 70 | |
| 45 | CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg | 626 |
| | 75 80 85 | |
| 50 | GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys | 674 |
| | 90 95 100 105 | |
| 55 | GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala | 722 |
| | 110 115 120 | |
| 60 | GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro | 770 |
| | 125 130 135 | |
| 65 | CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr | 818 |
| | 140 145 150 | |

0045516 102299

[illegible]

(5) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 10 (A) DESCRIPTION: B lymphocyte activation antigen; Ig
superfamily member; T cell costimulatory signal
via activation of CD28 pathways, binds to CD28⁺
T cells, transmembrane protein

15 (ix) FEATURE:

- (A) NAME/KEY: signal sequence
(B) LOCATION: -37 to -1
20 (C) IDENTIFICATION METHOD: similarity with known
sequence
(D) OTHER INFORMATION: hydrophobic

25 (ix) FEATURE:

- (A) NAME/KEY: extracellular domain
(B) LOCATION: 1 to 210
30 (C) IDENTIFICATION METHOD: similarity with known
sequence

(ix) FEATURE:

- 35 (A) NAME/KEY: transmembrane domain
(B) LOCATION: 211 to 235
(C) IDENTIFICATION METHOD: similarity with known
sequence

40 (ix) FEATURE:

- (A) NAME/KEY: intracellular (cytoplasmic) domain
(B) LOCATION: 236 to 269
45 (C) IDENTIFICATION METHOD: similarity with known
sequence

(ix) FEATURE:

- 50 (A) NAME/KEY: Ig V-set domain
(B) LOCATION: 1 to 105
(C) IDENTIFICATION METHOD: similarity with known
sequence

55

66201" 9153460

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain
 (B) LOCATION: 106 to 199
 5 (C) IDENTIFICATION METHOD: similarity with known
 sequence

(x) PUBLICATION INFORMATION:

- 10 (A) AUTHORS: FREEMAN, GORDON J.
 GRAY, GARY S.
 GIMMI, CLAUDE D.
 LOMBARD, DAVID B.
 15 ZHOU, LIANG-JI
 WHITE, MICHAEL
 FINGEROTH, JOYCE D.
 GRIBBEN, JOHN G.
 NADLER, LEE M.
 20 (B) TITLE: Structure, Expression, and T Cell Costimulatory
 Activity Of The Murine Homologue Of The Human B
 Lymphocyte Activation Antigen B7
 (C) JOURNAL: Journal of Experimental Medicine
 25 (D) VOLUME:
 (E) ISSUE:
 (F) PAGES:
 (G) DATE: IN PRESS
 (H) RELEVANT RESIDUES IN SEQUENCE ID NO:31: From -37 to 269
 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 -35 -30 -25
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 -20 -15 -10
 40 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 -5 -1 1 5 10
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 45 15 20 25
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 30 35 40
 50 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 45 50 55
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 60 65 70 75
 55

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|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Asp | Arg | Gly | Thr | Tyr | Ser | Cys | Val | Val | Gln | Lys | Lys | Glu | Arg | Gly | Thr | |
| | | | | | | 80 | | | | | 85 | | | | | 90 | |
| 5 | Tyr | Gly | Val | Lys | His | Leu | Ala | Leu | Val | Lys | Leu | Ser | Ile | Lys | Ala | Asp | |
| | | | | 95 | | | | | 100 | | | | | 105 | | | |
| | Phe | Ser | Thr | Pro | Asn | Ile | Thr | Glu | Ser | Gly | Asn | Pro | Ser | Ala | Asp | Thr | |
| | | | 110 | | | | | 115 | | | | | 120 | | | | |
| 10 | Lys | Arg | Ile | Thr | Cys | Phe | Ala | Ser | Gly | Gly | Phe | Pro | Lys | Pro | Arg | Phe | |
| | | 125 | | | | | 130 | | | | | 135 | | | | | |
| | Ser | Trp | Leu | Glu | Asn | Gly | Arg | Glu | Leu | Pro | Gly | Ile | Asn | Thr | Thr | Ile | |
| | 140 | | | | | 145 | | | | | 150 | | | | | 155 | |
| 15 | Ser | Gln | Asp | Pro | Glu | Ser | Glu | Leu | Tyr | Thr | Ile | Ser | Ser | Gln | Leu | Asp | |
| | | | | 160 | | | | | | 165 | | | | | 170 | | |
| | Phe | Asn | Thr | Thr | Arg | Asn | His | Thr | Ile | Lys | Cys | Leu | Ile | Lys | Tyr | Gly | |
| 20 | | | | 175 | | | | | 180 | | | | | 185 | | | |
| | Asp | Ala | His | Val | Ser | Glu | Asp | Phe | Thr | Trp | Glu | Lys | Pro | Pro | Glu | Asp | |
| | | | 190 | | | | | 195 | | | | | 200 | | | | |
| 25 | Pro | Pro | Asp | Ser | Lys | Asn | Thr | Leu | Val | Leu | Phe | Gly | Ala | Gly | Phe | Gly | |
| | | 205 | | | | | 210 | | | | | 215 | | | | | |
| | Ala | Val | Ile | Thr | Val | Val | Val | Ile | Val | Val | Ile | Ile | Lys | Cys | Phe | Cys | |
| | 220 | | | | | 225 | | | | | 230 | | | | | 235 | |
| 30 | Lys | His | Arg | Ser | Cys | Phe | Arg | Arg | Asn | Glu | Ala | Ser | Arg | Glu | Thr | Asn | |
| | | | | | 240 | | | | | 245 | | | | | 250 | | |
| | Asn | Ser | Leu | Thr | Phe | Gly | Pro | Glu | Glu | Ala | Leu | Ala | Glu | Gln | Thr | Val | |
| 35 | | | | 255 | | | | | 260 | | | | | 265 | | | |
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